

Serial No. 10/059,421
Docket No. YOR920010126US2

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REMARKS

Claims 31-60 are all the claims presently pending in the application. Claims 12 and 24 have been canceled and claims 31-60 have been added.

Applicant notes that newly added claims 31-60 are substantially the same as claims 1-30 which were presented in the Amendment filed herein on August 15, 2007.

It is noted that the claim amendments herein or later are not made to distinguish the invention over the prior art or narrow the claims or for any statutory requirements of patentability. Further, Applicant specifically states that no amendment to any claim herein or later should be construed as a disclaimer of any interest in or right to an equivalent of any element or feature of the amended claim.

Applicant respectfully submits that the claimed invention of claims 31-60 includes features that are not taught or suggested by the prior art.

In particular, Applicant would point out that an exemplary aspect of the claimed invention (e.g., as recited, for example, in claim 1) includes a processor which determines whether the open reading frame includes a putative gene **based on a number of the patterns of amino acids located in the amino acid translation of the ORF, and/or weighted values associated with the patterns of amino acids located in the amino acid translation of the ORF** (Application at page 13, lines 2-19). The exemplary aspects of the claimed invention may be considered as including the best characteristics of statistical approaches and database similarity searches, in identifying genes in a given DNA sequence (Application at page 6, lines 18-21).

Indeed, nowhere is this feature taught or suggested by Ganguly et al. (Proximal: A Database System for the Efficient Retrieval of Genetic Information", *Comput. Biol. Med.* Vol. 26, No 3, pp 199-207, 1996) (hereinafter "Ganguly") in view of Floratos et al. ("Sequence Homology Detection Through Large Scale Pattern Discovery", 1999) (hereinafter "Floratos"). In fact, the Examiner basically concedes that Ganguly does not teach or suggest this feature on page 3 of the Office Action.

The Examiner alleges that this feature is taught by Floratos. However, the Examiner is again incorrect.

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First, Applicant would point out that the title of the Floratos publication is "Sequence Homology Detection...". The title says nothing about "identifying genes" and in fact, the paper has nothing to do with identifying genes. Instead, as the title suggests, the publication deals with detecting similarities between a query sequence and a protein database.

Second, the Abstract states "[w]e describe a new approach for identifying sequence similarity between a query sequence and a data base of proteins" (emphasis added). Again, like the title, the Abstract says nothing about "identifying genes".

Third, the Floratos publication concludes with a Discussion which states "[w]e have presented here a methodology for performing similarity searches based on the discovery of patterns over an underlying database D of proteins and the use of these patterns for the identification of homologies between a query sequence and the proteins of the database at hand". Again, no mention of genes or identifying genes.

Indeed, the Examiner surprisingly attempts to rely on page 167, column 1, lines 17-41 to support his position. However, this passage simply deals with determining whether a pattern which has been discovered should be considered "significant". The passage has nothing to do with genes or identifying genes.

In fact, like the title, the Abstract, the Conclusion (e.g., Discussion), nowhere does this passage even mention genes and certainly does not mention identifying genes.

Moreover, nowhere in this passage or anywhere else, does Floratos teach or suggest a processor which determines whether the open reading frame includes a putative gene **based on a number of the patterns of amino acids located in the amino acid translation of the ORF, and/or weighted values associated with the patterns of amino acids located in the amino acid translation of the ORF.**

Therefore, Floratos clearly does not make up for the deficiencies of Ganguly.

Therefore, Applicant submits that these alleged references would not have been combined and even if combined, the combination would not teach or suggest each and every element of the claimed invention. Therefore, the Examiner is respectfully requested to withdraw this rejection.

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III. FORMAL MATTERS AND CONCLUSION

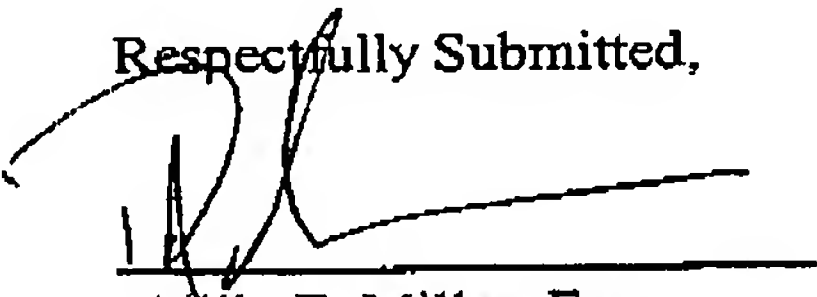
In view of the foregoing, Applicant submits that claims 31-60, all the claims presently pending in the application, are patentably distinct over the prior art of record and are in condition for allowance. The Examiner is respectfully requested to pass the above application to issue at the earliest possible time.

Should the Examiner find the application to be other than in condition for allowance, the Examiner is requested to contact the undersigned at the local telephone number listed below to discuss any other changes deemed necessary in a telephonic or personal interview.

The Commissioner is hereby authorized to charge any deficiency in fees or to credit any overpayment in fees to Assignee's Deposit Account No. 50-0510.

Respectfully Submitted,


Date: February 19, 2008


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CERTIFICATE OF FACSIMILE TRANSMISSION

I hereby certify that the foregoing was filed by facsimile with the United States Patent and Trademark Office, Examiner Cheyne D. Ly, Group Art Unit # 2168 at fax number (571) 273-8300 this 19th day of February, 2008.


Phillip E. Miller
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